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SEQUENCE LISTING

<110> Oregon State University

<120> Methods of use for infection-specific INCA, INCB, and INCC proteins of Chlamydia

<130> 52297

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<150> 60/082,588

<151> 1998-04-21

<150> 60/082,438

<151> 1998-04-20

<150> 60/086,450

<151> 1998-05-22

<160> 24

<170> PatentIn Ver. 2.0

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<212> DNA

<213> Chlamydia trachomatis

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1 5 10 15

aca ttt gca gct aat tct aca ggc aca att gga atc gtt aat tta cgt 96  
Thr Phe Ala Ala Asn Ser Thr Gly Thr Ile Gly Ile Val Asn Leu Arg  
20 25 30

cgc tgc cta gaa gag tct gct ctt ggg aaa aaa gaa tct gct gaa ttc 144  
Arg Cys Leu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe  
35 40 45

gaa aag atg aaa aac caa ttc tct aac agc atg ggg aag atg gag gaa 192  
Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu  
50 55 60

gaa ctg tct tct atc tat tcc aag ctc caa gac gac gat tac atg gaa 240  
Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu  
65 70 75 80

ggt cta tcc gag acc gca gct gcc gaa tta aga aaa aaa ttc gaa gat 288  
Gly Leu Ser Glu Thr Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp  
85 90 95

cta tct gca gaa tac aac aca gct caa ggg cag tat tac caa ata tta 336  
Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu

100

105

110

aac caa agt aat ttc aag cgc atg caa aag att atg gaa gaa gtg aaa 384  
 Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys  
 115 120 125

aaa gct tct gaa act gtg cgt att caa gaa ggc ttg tca gtc ctt ctt 432  
 Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu  
 130 135 140

aac gaa gat att gtc tta tct atc gat agt tcg gca gat aaa acc gat 480  
 Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp  
 145 150 155 160

gct gtt att aaa gtt ctt gat gtt ctt ttc aaa ata att aac atg cga 528  
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 165 170 175

agc tag 534  
 Ser

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Arg Cys Leu Glu Glu Ser Ala Leu Gly Lys Lys Glu Ser Ala Glu Phe  
 35 40 45

Glu Lys Met Lys Asn Gln Phe Ser Asn Ser Met Gly Lys Met Glu Glu  
 50 55 60

Glu Leu Ser Ser Ile Tyr Ser Lys Leu Gln Asp Asp Asp Tyr Met Glu  
 65 70 75 80

Gly Leu Ser Glu Thr Ala Ala Ala Glu Leu Arg Lys Lys Phe Glu Asp  
 85 90 95

Leu Ser Ala Glu Tyr Asn Thr Ala Gln Gly Gln Tyr Tyr Gln Ile Leu  
 100 105 110

Asn Gln Ser Asn Phe Lys Arg Met Gln Lys Ile Met Glu Glu Val Lys  
 115 120 125

Lys Ala Ser Glu Thr Val Arg Ile Gln Glu Gly Leu Ser Val Leu Leu  
 130 135 140

Asn Glu Asp Ile Val Leu Ser Ile Asp Ser Ser Ala Asp Lys Thr Asp  
 145 150 155 160

Ala Val Ile Lys Val Leu Asp Val Leu Phe Lys Ile Ile Asn Met Arg  
 165 170 175

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gtc	aag	aat	att	gtt	ctg	att	gat	gga	gcg	att	gat	cct	cat	tca	tat	96
Val	Lys	Asn	Ile	Val	Ile	Asp	Gly	Ala	Ile	Asp	Pro	His	Ser	Tyr		
20															30	

  

gag	atg	gtg	aag	ggg	gat	gaa	gac	cga	atg	gct	atg	agc	cag	ctg	att	144
Glu	Met	Val	Lys	Gly	Asp	Glu	Asp	Arg	Met	Ala	Met	Ser	Gln	Leu	Ile	
35															45	

  

ttt	tgc	aat	ggt	tta	ggt	tta	gag	cat	tca	gct	agt	tta	cgt	aaa	cat	192
Phe	Cys	Asn	Gly	Ile	Gly	Leu	Glu	His	Ser	Ala	Ser	Leu	Arg	Lys	His	
50															60	

  

cta	gag	ggt	aac	cca	aaa	gtc	gtt	gat	tta	ggt	caa	cgt	ttg	ctt	aac	240
Leu	Glu	Gly	Asn	Pro	Lys	Val	Val	Asp	Leu	Gly	Gln	Arg	Leu	Leu	Asn	
65															80	

  

aaa	aac	tgt	ttt	gat	ctt	ctg	agt	gaa	gaa	gga	ttc	cct	gac	cca	cat	288
Lys	Asn	Cys	Phe	Asp	Leu	Ile	Ser	Glu	Glu	Gly	Phe	Pro	Asp	Pro	His	
85															95	

  

att	tgg	acg	gat	atg	aga	gta	tgg	ggt	gct	gct	gta	aaa	gag	atg	gct	336
Ile	Trp	Thr	Asp	Met	Arg	Val	Trp	Gly	Ala	Ala	Val	Lys	Glu	Met	Ala	
100															110	

  

gcg	gca	tta	att	caa	caa	ttt	cct	caa	tat	gaa	gaa	gat	ttt	caa	aag	384
Ala	Ala	Leu	Ile	Gln	Gln	Phe	Pro	Gln	Tyr	Glu	Glu	Asp	Phe	Gln	Lys	
115															125	

  

aat	gcg	gat	cag	atc	tta	tca	gag	atg	gag	gaa	ctt	gat	cgt	tgg	gca	432
Asn	Ala	Asp	Gln	Ile	Leu	Ser	Glu	Met	Glu	Glu	Leu	Asp	Arg	Trp	Ala	
130															140	

  

gtg	cgt	tct	ctc	tct	acg	att	cct	gaa	aaa	aat	cgc	tat	tta	gtc	aca	480
Val	Arg	Ser	Leu	Ser	Thr	Ile	Pro	Glu	Lys	Asn	Arg	Tyr	Leu	Val	Thr	
145															160	

  

ggc	cac	aat	gcg	ttc	agt	tac	ttt	act	cgt	cg	tat	cta	tcc	tct	gat	528
Gly	His	Asn	Ala	Phe	Ser	Tyr	Phe	Thr	Arg	Arg	Tyr	Leu	Ser	Ser	Asp	
165															175	

  

gcg	gag	aga	gtg	tct	ggg	gaa	tgg	aga	tcg	cgt	tgc	att	tct	cca	gaa	576
Ala	Glu	Arg	Val	Ser	Gly	Glu	Trp	Arg	Ser	Arg	Cys	Ile	Ser	Pro	Glu	
180															190	

WO 99/53948

PCT/US99/08744

ggg ttg tct cct gag gct cag att agt atc cga gat att atg cgt gta	624
Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val	
195 200 205	
gtg gag tat atc tct gca aac gat gta gaa gtt gtc ttt tta gag gat	672
Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp	
210 215 220	
acg tta aat caa gat gct ttg aga aag att gtt tct tgc tct aag agc	720
Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser	
225 230 235 240	
gga caa aag att cgt ctc gct aag tct cct tta tat agc gat aat gtc	768
Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val	
245 250 255	
tgt gat aac tat ttt agc acg ttc cag cac aat gtt cgc aca att aca	816
Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr	
260 265 270	
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Glu Met Val Lys Gly Asp Glu Asp Arg Met Ala Met Ser Gln Leu Ile	
35 40 45	
Phe Cys Asn Gly Leu Gly Leu Glu His Ser Ala Ser Leu Arg Lys His	
50 55 60	
Leu Glu Gly Asn Pro Lys Val Val Asp Leu Gly Gln Arg Leu Leu Asn	
65 70 75 80	
Lys Asn Cys Phe Asp Leu Leu Ser Glu Glu Gly Phe Pro Asp Pro His	
85 90 95	
Ile Trp Thr Asp Met Arg Val Trp Gly Ala Ala Val Lys Glu Met Ala	
100 105 110	
Ala Ala Leu Ile Gln Gln Phe Pro Gln Tyr Glu Glu Asp Phe Gln Lys	
115 120 125	
Asn Ala Asp Gln Ile Leu Ser Glu Met Glu Glu Leu Asp Arg Trp Ala	
130 135 140	
Val Arg Ser Leu Ser Thr Ile Pro Glu Lys Asn Arg Tyr Leu Val Thr	
145 150 155 160	

WO 99/53948

PCT/US99/08744

Gly His Asn Ala Phe Ser Tyr Phe Thr Arg Arg Tyr Leu Ser Ser Asp  
165 170 175

Ala Glu Arg Val Ser Gly Glu Trp Arg Ser Arg Cys Ile Ser Pro Glu  
180 185 190

Gly Leu Ser Pro Glu Ala Gln Ile Ser Ile Arg Asp Ile Met Arg Val  
195 200 205

Val Glu Tyr Ile Ser Ala Asn Asp Val Glu Val Val Phe Leu Glu Asp  
210 215 220

Thr Leu Asn Gln Asp Ala Leu Arg Lys Ile Val Ser Cys Ser Lys Ser  
225 230 235 240

Gly Gln Lys Ile Arg Leu Ala Lys Ser Pro Leu Tyr Ser Asp Asn Val  
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Cys Asp Asn Tyr Phe Ser Thr Phe Gln His Asn Val Arg Thr Ile Thr  
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Glu Glu Leu Gly Gly Thr Val Leu Glu  
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tta cag aag aat tgg gag gga ctg ttc ttg aat aga gat aat gca att 96  
Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asp Asn Ala Ile  
20 25 30

gct tgg tcc gta gag gat ctt tgt gtt aat tat gat cac tca gac gtc 144  
Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val  
35 40 45

tta tgt cac att act ttt tct ctg cct gca ggg gca atg gct gct att 192  
Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile  
50 55 60

att ggg ccg aat gga gct ggt aaa agt act ttg ctt aag gct tct tta 240  
Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu  
65 70 75 80

gga ctg att cgt gct tct ggc caa agc ttg ttc ttt ggt cag aga 288  
Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg  
85 90 95

ttt tcc aag gca cat cat aga ata gcc tat atg cct caa aga gcg agt 336  
Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser

100

105

110

gtg gat tgg gat ttc cca atg act gtt ctt gat ctc gtg ttg atg ggg 384  
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 115 120 125

tgt tac ggc tat aaa gga ata tgg aat cgt att tcc act gat gat cgt 432  
 Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg  
 130 135 140

cag gag gct atg cgt att tta gag cgg gtt ggt ttg gaa gct ttt gca 480  
 Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala  
 145 150 155 160

aat cgt caa ata ggt aag ctc tct gga gga caa caa cag aga gct ttt 528  
 Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Arg Ala Phe  
 165 170 175

tta gcg cgg tca tta atg caa aaa gca gat ttg tat ctc atg gat gag 576  
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 180 185 190

ctg ttc tct gcg atc gat atg gcc tct tat cag atg gtt gta gat gtt 624  
 Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val  
 195 200 205

ttg caa gag ctt aaa agc gaa ggg aag act att gtg gtc att cat cat 672  
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 210 215 220

gat ttg agt aat gtc cgg aag ctt ttt gat cat gtg att tta tta aat 720  
 Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn  
 225 230 235 240

aag cat ctt gtg tgc tct gga agc gta gaa gaa tgc ttg act aaa gaa 768  
 Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu  
 245 250 255

gcc att ttt cag gct tat ggg tgt gac ttg agc ttt tgg att aca cac 816  
 Ala Ile Phe Gln Ala Tyr Gly Cys Asp Leu Ser Phe Trp Ile Thr His  
 260 265 270

tca aat tgt cta gag gca agt acc aag gat cgt gct aga tgc tga 861  
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&lt;211&gt; 286

&lt;212&gt; PRT

&lt;213&gt; Chlamydia trachomatis

&lt;400&gt; 6

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Leu Gln Lys Asn Trp Glu Gly Leu Phe Leu Asn Arg Asp Asn Ala Ile  
 20 25 30

Ala Trp Ser Val Glu Asp Leu Cys Val Asn Tyr Asp His Ser Asp Val  
 35 40 45

WO 99/53948

PCT/US99/08744

Leu Cys His Ile Thr Phe Ser Leu Pro Ala Gly Ala Met Ala Ala Ile  
50 55 60

Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Ala Ser Leu  
65 70 75 80

Gly Leu Ile Arg Ala Ser Ser Gly Gln Ser Leu Phe Phe Gly Gln Arg  
85 90 95

Phe Ser Lys Ala His His Arg Ile Ala Tyr Met Pro Gln Arg Ala Ser  
100 105 110

Val Asp Trp Asp Phe Pro Met Thr Val Leu Asp Leu Val Leu Met Gly  
115 120 125

Cys Tyr Gly Tyr Lys Gly Ile Trp Asn Arg Ile Ser Thr Asp Asp Arg  
130 135 140

Gln Glu Ala Met Arg Ile Leu Glu Arg Val Gly Leu Glu Ala Phe Ala  
145 150 155 160

Asn Arg Gln Ile Gly Lys Leu Ser Gly Gly Gln Gln Arg Ala Phe  
165 170 175

Leu Ala Arg Ser Leu Met Gln Lys Ala Asp Leu Tyr Leu Met Asp Glu  
180 185 190

Leu Phe Ser Ala Ile Asp Met Ala Ser Tyr Gln Met Val Val Asp Val  
195 200 205

Leu Gln Glu Leu Lys Ser Glu Gly Lys Thr Ile Val Val Ile His His  
210 215 220

Asp Leu Ser Asn Val Arg Lys Leu Phe Asp His Val Ile Leu Leu Asn  
225 230 235 240

Lys His Leu Val Cys Ser Gly Ser Val Glu Glu Cys Leu Thr Lys Glu  
245 250 255

Ala Ile Phe Gln Ala Tyr Gly Cys Asp Leu Ser Phe Trp Ile Thr His  
260 265 270

Ser Asn Cys Leu Glu Ala Ser Thr Lys Asp Arg Ala Arg Cys  
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<212> DNA

<213> Chlamydia psittaci

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tca cct act ttt gga gat cat ggt aag gat ttc gac aac aat aaa att	96
Ser Pro Thr Phe Gly Asp His Gly Lys Asp Phe Asp Asn Asn Lys Ile	
20 25 30	
ata ccc att tca ata gaa gct cca act tct tca gct gct gta ggg	144
Ile Pro Ile Ser Ile Glu Ala Pro Thr Ser Ser Ala Ala Ala Val Gly	
35 40 45	
gct aaa acg gct atc gag cct gaa gga aga agc cca cta ctt caa agg	192
Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg	
50 55 60	
att tgc tat ctt gtt aaa att atc gct gcc atc gcc ctc ttt gtt gtt	240
Ile Cys Tyr Leu Val Lys Ile Ala Ala Ile Ala Leu Phe Val Val	
65 70 75 80	
ggt atc gca gcc tta gtt tgc tta tat ctc ggt agc gtt atc tca acg	288
Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr	
85 90 95	
cct tct ctt att ctt atg ctt gcg atc atg ctt gta tcc ttt gtg atc	336
Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile	
100 105 110	
gtt att acg gca att cga gat ggc aca ccg tct caa gtg gtc cgt cac	384
Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His	
115 120 125	
atg aaa cag caa att cag caa ttt ggc gaa gaa aac acg cgt tta cat	432
Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His	
130 135 140	
acc gca gta gaa aat cta aaa gct gtt aac gtt gag ctc tca gag caa	480
Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln	
145 150 155 160	
att aac caa ctt aaa caa cta cat act aga tta tcg gat ttt ggt gat	528
Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp	
165 170 175	
agg ctt gaa gcg aat acc ggt gat ttt act gca ctt att gcg gat ttc	576
Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe	
180 185 190	
caa ctc agt ctg gaa gag ttt aag tct gtt ggt act aaa gtt gaa acc	624
Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr	
195 200 205	
atg ctc tct cca ttt gag aaa tta gct cag tct ttg aaa gag acc ttt	672
Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe	
210 215 220	
tct caa gaa gct gtt cag gca atg atg tcc tct gta act gag tta aga	720
Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg	
225 230 235 240	
acc aat ttg aat gca ttg aaa gag ctt ata aca gag aat aaa acc gta	768
Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val	
245 250 255	
ata gag caa cta aaa gct gat gct caa ctt aga gaa gag caa gtg cgg	816

Ile Glu Gln Leu Lys Ala Asp Ala Gln Leu Arg Glu Glu Gln Val Arg	260	265	270	
ttt tta gaa aag cgt aaa caa gag tta gaa gag gct tgg tca aca ttg	275	280	285	864
Phe Leu Glu Lys Arg Lys Gln Glu Leu Glu Ala Cys Ser Thr Leu				
tcc cat tca att gcg act cta cag gaa tcc aca acc ctt cta aag gac	290	295	300	912
Ser His Ser Ile Ala Thr Leu Gln Glu Ser Thr Thr Leu Leu Lys Asp				
tct aca act aac tta cat gca gtt gaa agt cgt ctt atc ggt gtt atg	305	310	315	960
Ser Thr Thr Asn Leu His Ala Val Glu Ser Arg Leu Ile Gly Val Met				
gtt cag gat ggt gca gag tcc tcc acc gta gag gaa gct tca caa gat	325	330	335	1008
Val Gln Asp Gly Ala Glu Ser Ser Thr Val Glu Glu Ala Ser Gln Asp				
gat agc gcg caa ccc caa gat gaa aat caa tct gat gct gga gag cat	340	345	350	1056
Asp Ser Ala Gln Pro Gln Asp Glu Asn Gln Ser Asp Ala Gly Glu His				
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Lys Asp Ser				
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<213> Chlamydia psittaci				
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Ser Pro Thr Phe Gly Asp His Gly Lys Asp Phe Asp Asn Asn Lys Ile	20	25	30	
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Ala Lys Thr Ala Ile Glu Pro Glu Gly Arg Ser Pro Leu Leu Gln Arg	50	55	60	
Ile Cys Tyr Leu Val Lys Ile Ile Ala Ala Ile Ala Leu Phe Val Val	65	70	75	80
Gly Ile Ala Ala Leu Val Cys Leu Tyr Leu Gly Ser Val Ile Ser Thr	85	90	95	
Pro Ser Leu Ile Leu Met Leu Ala Ile Met Leu Val Ser Phe Val Ile	100	105	110	
Val Ile Thr Ala Ile Arg Asp Gly Thr Pro Ser Gln Val Val Arg His	115	120	125	
Met Lys Gln Gln Ile Gln Gln Phe Gly Glu Glu Asn Thr Arg Leu His	130	135	140	

WO 99/53948

PCT/US99/08744

Thr Ala Val Glu Asn Leu Lys Ala Val Asn Val Glu Leu Ser Glu Gln  
145 150 155 160

Ile Asn Gln Leu Lys Gln Leu His Thr Arg Leu Ser Asp Phe Gly Asp  
165 170 175

Arg Leu Glu Ala Asn Thr Gly Asp Phe Thr Ala Leu Ile Ala Asp Phe  
180 185 190

Gln Leu Ser Leu Glu Glu Phe Lys Ser Val Gly Thr Lys Val Glu Thr  
195 200 205

Met Leu Ser Pro Phe Glu Lys Leu Ala Gln Ser Leu Lys Glu Thr Phe  
210 215 220

Ser Gln Glu Ala Val Gln Ala Met Met Ser Ser Val Thr Glu Leu Arg  
225 230 235 240

Thr Asn Leu Asn Ala Leu Lys Glu Leu Ile Thr Glu Asn Lys Thr Val  
245 250 255

Ile Glu Gln Leu Lys Ala Asp Ala Gln Leu Arg Glu Glu Gln Val Arg  
260 265 270

Phe Leu Glu Lys Arg Lys Gln Glu Leu Glu Glu Ala Cys Ser Thr Leu  
275 280 285

Ser His Ser Ile Ala Thr Leu Gln Glu Ser Thr Thr Leu Leu Lys Asp  
290 295 300

Ser Thr Thr Asn Leu His Ala Val Glu Ser Arg Leu Ile Gly Val Met  
305 310 315 320

Val Gln Asp Gly Ala Glu Ser Ser Thr Val Glu Glu Ala Ser Gln Asp  
325 330 335

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340 345 350

Lys Asp Ser  
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<212> DNA

<213> Chlamydia psittaci

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gac gtt tta ata gct ttt aat aga aag cta aat ctc gta gaa caa caa 96  
Asp Val Leu Ile Ala Phe Asn Arg Lys Leu Asn Leu Val Glu Gln Gln  
20 25 30

gcg aaa gaa ctt gaa acg aaa gtc agt ttg gta gac aga aca gct act 144  
 Ala Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr  
 35 40 45

tta tca ctt acc act ggc aat aat gta gcc acg gat gta ctc ctt tta 192  
 Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu Leu  
 50 55 60

aaa gat gag gtt gca gaa cta aaa gga tgt ttg tct gca gtt acg gat 240  
 Lys Asp Glu Val Ala Glu Leu Lys Gly Cys Leu Ser Ala Val Thr Asp  
 65 70 75 80

cta tta atc cgc tca ggc tca tca aga aca cct ggg ggt gct cct aat 288  
 Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn  
 85 90 95

cca gaa ggc act aat tac cta ata gga tgc aca cct cct tct ctt tgc 336  
 Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys  
 100 105 110

gct aaa ctt aca gcg tta gcg tta aca att ata gcc ctc att gct atc 384  
 Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile  
 115 120 125

aca gta ctt gtt atc tgt att gtt act gtt tgc ggc ggt ttc ccc cta 432  
 Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu  
 130 135 140

ttt att tcc cta ctc aac atg tac aca gtt ggt gct tgt ata tcc tta 480  
 Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu  
 145 150 155 160

ccg atc att tcg tgt gcc gca gtt tca atg atg att cta tgc tca cat 528  
 Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His  
 165 170 175

tct att aac tct tta tta aga aac agg cct gcg atc tat atg act aac 576  
 Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn  
 180 185 190

aat ttt caa aca gaa tct taa 597  
 Asn Phe Gln Thr Glu Ser  
 195

<210> 10  
 <211> 198  
 <212> PRT  
 <213> Chlamydia psittaci

<400> 10  
 Met Ser Thr Thr Pro Ala Ser Ser Ala Ser Arg Asp Val Leu Leu Asp  
 1 5 10 15

Asp Val Leu Ile Ala Phe Asn Arg Lys Leu Asn Leu Val Glu Gln Gln  
 20 25 30

Ala Lys Glu Leu Glu Thr Lys Val Ser Leu Val Asp Arg Thr Ala Thr  
 35 40 45

Leu Ser Leu Thr Thr Gly Asn Asn Val Ala Thr Asp Val Leu Leu Leu

50

55

60

Lys Asp Glu Val Ala Glu Leu Lys Gly Cys Leu Ser Ala Val Thr Asp  
 65 70 75 80

Leu Leu Ile Arg Ser Gly Ser Ser Arg Thr Pro Gly Gly Ala Pro Asn  
 85 90 95

Pro Glu Gly Thr Asn Tyr Leu Ile Gly Cys Thr Pro Pro Ser Leu Cys  
 100 105 110

Ala Lys Leu Thr Ala Leu Ala Leu Thr Ile Ile Ala Leu Ile Ala Ile  
 115 120 125

Thr Val Leu Val Ile Cys Ile Val Thr Val Cys Gly Gly Phe Pro Leu  
 130 135 140

Phe Ile Ser Leu Leu Asn Met Tyr Thr Val Gly Ala Cys Ile Ser Leu  
 145 150 155 160

Pro Ile Ile Ser Cys Ala Ala Val Ser Met Met Ile Leu Cys Ser His  
 165 170 175

Ser Ile Asn Ser Leu Leu Arg Asn Arg Pro Ala Ile Tyr Met Thr Asn  
 180 185 190

Asn Phe Gln Thr Glu Ser  
 195

<210> 11

<211> 561

<212> DNA

<213> Chlamydia psittaci

<220>

<221> CDS

<222> (1)...(561)

<400> 11

atg acc tct gta aga acc gat tta act cca ggc gac acc tca ctc caa 48  
 Met Thr Ser Val Arg Thr Asp Leu Thr Pro Gly Asp Thr Ser Leu Gln  
 1 5 10 15

tct tct tta tta aat ccg agt gat ctc aca aca caa cta tcc aac ctc 96  
 Ser Ser Leu Leu Asn Pro Ser Asp Leu Thr Thr Gln Leu Ser Asn Leu  
 20 25 30

cag act gtt ctc gca ggg ata caa caa caa cat cct tta aac ggt ggt 144  
 Gln Thr Val Leu Ala Gly Ile Gln Gln Gln His Pro Leu Asn Gly Gly  
 35 40 45

tgg cct cag cat cat cct act ggc gct gca gat caa aat tat ctc atg 192  
 Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met  
 50 55 60

cgt ctg atg caa tct cat atg gca agt acc gta tca gca gta tct gaa 240  
 Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu  
 65 70 75 80

tta aga acc gaa gtc act gca atc aag aca aaa ttg cac ggg cta tct 288

Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser	85	90	95	
act cca gct aat gtt tgc agc ggt cct atg gct cta gcc gct ttt ctt				336
Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Ala Phe Leu	100	105	110	
cta gct ata tct tta gtt gcg att atc atc att gtt tta gcc tcc tta				384
Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu	115	120	125	
ggc ctt gca ggc ata cta cct caa gct gcc gct atc tta gtg aat aca				432
Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ile Leu Val Asn Thr	130	135	140	
gca aac tct ata tgg gct att gtt agc gct tcg ata gtc act gtt atc				480
Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile	145	150	155	160
tgc tta att agc gtg cta tgc ata acg cta att cga cac cat aaa ccc				528
Cys Leu Ile Ser Val Leu Cys Ile Thr Leu Ile Arg His His Lys Pro	165	170	175	
tta cct att gaa act agg cct acc gga cat taa				561
Leu Pro Ile Glu Thr Arg Pro Thr Gly His	180	185		
<210> 12				
<211> 186				
<212> PRT				
<213> Chlamydia psittaci				
<400> 12				
Met Thr Ser Val Arg Thr Asp Leu Thr Pro Gly Asp Thr Ser Leu Gln	1	5	10	15
Ser Ser Leu Leu Asn Pro Ser Asp Leu Thr Thr Gln Leu Ser Asn Leu	20	25	30	
Gln Thr Val Leu Ala Gly Ile Gln Gln His Pro Leu Asn Gly Gly	35	40	45	
Trp Pro Gln His His Pro Thr Gly Ala Ala Asp Gln Asn Tyr Leu Met	50	55	60	
Arg Leu Met Gln Ser His Met Ala Ser Thr Val Ser Ala Val Ser Glu	65	70	75	80
Leu Arg Thr Glu Val Thr Ala Ile Lys Thr Lys Leu His Gly Leu Ser	85	90	95	
Thr Pro Ala Asn Val Cys Ser Gly Pro Met Ala Leu Ala Ala Phe Leu	100	105	110	
Leu Ala Ile Ser Leu Val Ala Ile Ile Ile Val Leu Ala Ser Leu	115	120	125	
Gly Leu Ala Gly Ile Leu Pro Gln Ala Ala Ile Leu Val Asn Thr	130	135	140	

Ala Asn Ser Ile Trp Ala Ile Val Ser Ala Ser Ile Val Thr Val Ile  
 145 150 155 160

Cys Leu Ile Ser Val Leu Cys Ile Thr Leu Ile Arg His His Lys Pro  
 165 170 175

Leu Pro Ile Glu Thr Arg Pro Thr Gly His  
 180 185

<210> 13

<211> 822

<212> DNA

<213> Chlamydia trachomatis

<220>

<221> CDS

<222> (1)...(822)

<400> 13

atg aca acg cct act cta atc gtg att cct cca tct ccc cct gca cct 48  
 Met Thr Thr Pro Thr Leu Ile Val Ile Pro Pro Ser Pro Pro Ala Pro  
 1 5 10 15

tcc tac tca gcc aat cgc gta cct caa cct tct ttg atg gac aaa att 96  
 Ser Tyr Ser Ala Asn Arg Val Pro Gln Pro Ser Leu Met Asp Lys Ile  
 20 25 30

aag aaa ata gca gcc att gcc tcc cta att ctt ata ggc aca ata ggc 144  
 Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly  
 35 40 45

ttt tta gct ctt ttg gga cat ctt gtt ggc ttt ctg atc gct cca caa 192  
 Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln  
 50 55 60

atc act att gtt ctt ctt gcc cta ttc att acc tca tta gca ggg aat 240  
 Ile Thr Ile Val Leu Leu Ala Leu Phe Ile Thr Ser Leu Ala Gly Asn  
 65 70 75 80

gct ctt tat cta cag aaa acc gct aat cta cat cta tac cag gat ctg 288  
 Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu  
 85 90 95

caa aga gaa gtt ggg tct cta aaa gaa att aat ttc atg ctg agc gtt 336  
 Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val  
 100 105 110

cta cag aaa gaa ttt ctt cat tta tct aaa gaa ttt gca acg aca tct 384  
 Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Thr Ser  
 115 120 125

aaa gac ctc tct gct gta tct caa gat ttt tat tct tgt ttg caa gga 432  
 Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly  
 130 135 140

ttt aga gat aac tat aaa ggt ttt gaa tct ctt ttg gat gag tat aaa 480  
 Phe Arg Asp Asn Tyr Lys Gly Phe Glu Ser Leu Leu Asp Glu Tyr Lys  
 145 150 155 160

aac tct aca gaa gaa atg cgc aaa ctc ttt tcg caa gaa atc ata gca 528

Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala			
165	170	175	
gat ctt aaa ggc tct gtt gcc tca tta aga gag gaa atc cga ttc cta		576	
Asp Leu Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu			
180	185	190	
acc cca tta gca gaa gaa gtt cgc cga tta gcg cat aac cag gaa tca		624	
Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser			
195	200	205	
tta aca gcg gct att gaa gaa tta aaa aca att cgt gat agc tta cga		672	
Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg			
210	215	220	
gat gaa att gga caa ctt tca caa ctt tct aaa act ctt acc agt caa		720	
Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln			
225	230	235	240
att gca tta caa cga aaa gag agc tca gat ctg tgt tcc cag ata aga		768	
Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg			
245	250	255	
gag acg ctc tcc tcc ccc aga aag tct gca tca ccc tct aca aaa agc		816	
Glu Thr Leu Ser Ser Pro Arg Lys Ser Ala Ser Pro Ser Thr Lys Ser			
260	265	270	
tcc tag		822	
Ser			
<210> 14			
<211> 273			
<212> PRT			
<213> Chlamydia trachomatis			
<400> 14			
Met Thr Thr Pro Thr Leu Ile Val Ile Pro Pro Ser Pro Pro Ala Pro			
1	5	10	15
Ser Tyr Ser Ala Asn Arg Val Pro Gln Pro Ser Leu Met Asp Lys Ile			
20	25	30	
Lys Lys Ile Ala Ala Ile Ala Ser Leu Ile Leu Ile Gly Thr Ile Gly			
35	40	45	
Phe Leu Ala Leu Leu Gly His Leu Val Gly Phe Leu Ile Ala Pro Gln			
50	55	60	
Ile Thr Ile Val Leu Leu Ala Leu Phe Ile Thr Ser Leu Ala Gly Asn			
65	70	75	80
Ala Leu Tyr Leu Gln Lys Thr Ala Asn Leu His Leu Tyr Gln Asp Leu			
85	90	95	
Gln Arg Glu Val Gly Ser Leu Lys Glu Ile Asn Phe Met Leu Ser Val			
100	105	110	
Leu Gln Lys Glu Phe Leu His Leu Ser Lys Glu Phe Ala Thr Thr Ser			
115	120	125	

WO 99/53948

PCT/US99/08744

Lys Asp Leu Ser Ala Val Ser Gln Asp Phe Tyr Ser Cys Leu Gln Gly  
130 135 140

Phe Arg Asp Asn Tyr Lys Gly Phe Glu Ser Leu Leu Asp Glu Tyr Lys  
145 150 155 160

Asn Ser Thr Glu Glu Met Arg Lys Leu Phe Ser Gln Glu Ile Ile Ala  
165 170 175

Asp Leu Lys Gly Ser Val Ala Ser Leu Arg Glu Glu Ile Arg Phe Leu  
180 185 190

Thr Pro Leu Ala Glu Glu Val Arg Arg Leu Ala His Asn Gln Glu Ser  
195 200 205

Leu Thr Ala Ala Ile Glu Glu Leu Lys Thr Ile Arg Asp Ser Leu Arg  
210 215 220

Asp Glu Ile Gly Gln Leu Ser Gln Leu Ser Lys Thr Leu Thr Ser Gln  
225 230 235 240

Ile Ala Leu Gln Arg Lys Glu Ser Ser Asp Leu Cys Ser Gln Ile Arg  
245 250 255

Glu Thr Leu Ser Ser Pro Arg Lys Ser Ala Ser Pro Ser Thr Lys Ser  
260 265 270

Ser

<210> 15

<211> 348

<212> DNA

<213> Chlamydia trachomatis

<220>

<221> CDS

<222> (1)..(348)

<400> 15

atg gtt cat tct gta tac aat tca ttg gct cca gaa ggt ttt agc caa 48  
Met Val His Ser Val Tyr Asn Ser Leu Ala Pro Glu Gly Phe Ser Gln  
1 5 10 15

gtc tct att caa ccc agt cag att cca acc agc aaa aaa gta atg att 96  
Val Ser Ile Gln Pro Ser Gln Ile Pro Thr Ser Lys Lys Val Met Ile  
20 25 30

gcg ata atg act ctt ttt gca ctc aca gcc att gca gca ata gtc ctt 144  
Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ala Ile Val Leu  
35 40 45

tcc atc gtt aca gtt tgt gga ggg ttt cct ttt ctt ctt gct gca ctt 192  
Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu  
50 55 60

aac acc gta act att ggt gca tgc gta tcc ttg ccg gta ttc act tgc 240  
Asn Thr Val Thr Ile Gly Ala Cys Val Ser Leu Pro Val Phe Thr Cys  
65 70 75 80

ata gct aca acg tta tta ctt ctt tgt ctc cgt aat atc gaa ctc cta 288

WO 99/53948

PCT/US99/08744

Ile Ala Thr Thr Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu  
85 90 95

gcc aga ccg caa gta ttt acc ctc tcc act caa ttc agc cca aca aaa 336  
Ala Arg Pro Gln Val Phe Thr Leu Ser Thr Gln Phe Ser Pro Thr Lys  
100 105 110

cct caa gaa tag 348  
Pro Gln Glu  
115

<210> 16  
<211> 115  
<212> PRT  
<213> Chlamydia trachomatis

<400> 16  
Met Val His Ser Val Tyr Asn Ser Leu Ala Pro Glu Gly Phe Ser Gln  
1 5 10 15

Val Ser Ile Gln Pro Ser Gln Ile Pro Thr Ser Lys Lys Val Met Ile  
20 25 30

Ala Ile Met Thr Leu Phe Ala Leu Thr Ala Ile Ala Ala Ile Val Leu  
35 40 45

Ser Ile Val Thr Val Cys Gly Gly Phe Pro Phe Leu Leu Ala Ala Leu  
50 55 60

Asn Thr Val Thr Ile Gly Ala Cys Val Ser Leu Pro Val Phe Thr Cys  
65 70 75 80

Ile Ala Thr Thr Leu Leu Leu Cys Leu Arg Asn Ile Glu Leu Leu  
85 90 95

Ala Arg Pro Gln Val Phe Thr Leu Ser Thr Gln Phe Ser Pro Thr Lys  
100 105 110

Pro Gln Glu  
115

<210> 17  
<211> 537  
<212> DNA  
<213> Chlamydia trachomatis

<220>  
<221> CDS  
<222> (1)...(537)

<400> 17  
atg acg tac tct ata tcc gat ata gca cac aaa tct gat att tct aat 48  
Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn  
1 5 10 15

ccc acg tct ccc gct cca tca aga aaa cga gga tcc ttt ccc cca caa 96  
Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln  
20 25 30

tct cct tct gcc gtg ggc tct tta gag gga gct aat ttc tct aca tgg	144
Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp	
35 40 45	
ggg cca ggc ccc ttc ttc act gtc cct gtt tat cca caa caa ctc gct	192
Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala	
50 55 60	
gca atg caa aac aac ctt ttt aca ttg caa aca gag gtt tct gct ctc	240
Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu	
65 70 75 80	
aag aaa aaa tta gtt cag tct agt cag aca cgc gga tct tta gga ctc	288
Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu	
85 90 95	
ggc ccg cag ttt tta gcg gca tgc tta gtt gct gcg aca atc ctt gca	336
Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala	
100 105 110	
gta gct gtt atc gta ctt gct tcc tta gga ctt ggc ggt gtt ctt cct	384
Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Gly Val Leu Pro	
115 120 125	
ttt gtc ctt gtt tgt ctg gct ggg tca act aat gca att tgg gct att	432
Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile	
130 135 140	
gtg agc gcc tcc atc act aca ctg att tgt tgc gtt tcc atc gct tgc	480
Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys	
145 150 155 160	
atc ttc tta gca aaa tgt gat aag gga tct gat cct caa act tta tat	528
Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr	
165 170 175	
gta agc taa	537
Val Ser	
<210> 18	
<211> 178	
<212> PRT	
<213> Chlamydia trachomatis	
<400> 18	
Met Thr Tyr Ser Ile Ser Asp Ile Ala His Lys Ser Asp Ile Ser Asn	
1 5 10 15	
Pro Thr Ser Pro Ala Pro Ser Arg Lys Arg Gly Ser Phe Pro Pro Gln	
20 25 30	
Ser Pro Ser Ala Val Gly Ser Leu Glu Gly Ala Asn Phe Ser Thr Trp	
35 40 45	
Gly Pro Gly Pro Phe Phe Thr Val Pro Val Tyr Pro Gln Gln Leu Ala	
50 55 60	
Ala Met Gln Asn Asn Leu Phe Thr Leu Gln Thr Glu Val Ser Ala Leu	
65 70 75 80	

Lys Lys Lys Leu Val Gln Ser Ser Gln Thr Arg Gly Ser Leu Gly Leu  
85 90 95

Gly Pro Gln Phe Leu Ala Ala Cys Leu Val Ala Ala Thr Ile Leu Ala  
100 105 110

Val Ala Val Ile Val Leu Ala Ser Leu Gly Leu Gly Gly Val Leu Pro  
115 120 125

Phe Val Leu Val Cys Leu Ala Gly Ser Thr Asn Ala Ile Trp Ala Ile  
130 135 140

Val Ser Ala Ser Ile Thr Thr Leu Ile Cys Cys Val Ser Ile Ala Cys  
145 150 155 160

Ile Phe Leu Ala Lys Cys Asp Lys Gly Ser Asp Pro Gln Thr Leu Tyr  
165 170 175

Val Ser

<210> 19

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 19

agaaccgatt taactccagg cg

22

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 20

gcgcggatcc ttaatgtccg gtaggcctag

30

<210> 21

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 21

atgtcaacaa caccagcatc ttc

23

<210> 22

<211> 34

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
<400> 22  
gcgcggatcc ttaattatgt ctttctggat tagg

34

<210> 23  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
<400> 23  
cgcagtactg tatccacaga caac

24

<210> 24  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer  
<400> 24  
gtcggatccg agaaaactctc catgcc

26